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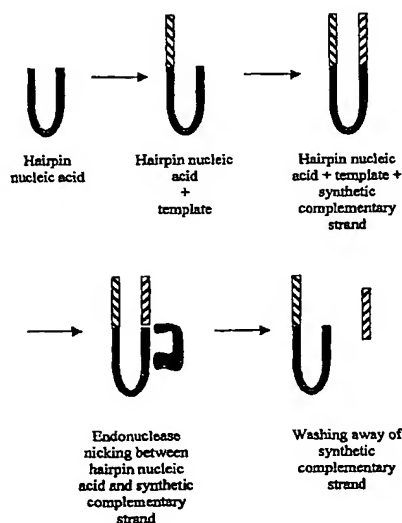
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(57) Abstract: The invention relates to a method of detecting the precise locations of methyl-cytosines in a given nucleic acid sequence. In particular, the invention features a method which includes sequencing a template nucleic acid that is attached to a hairpin nucleic acid or double-stranded nucleic acid anchor, which contain specifically-designed sites for nicking or other endonucleases. The template nucleic acid is then regenerated to single-stranded form via methods described herein, and then treated to convert either the methylated cytosines, or non-methylated cytosines, and the template nucleic acid is then re-sequenced. The results of the first and second sequencing reactions are then compared.